

Sequences producing significant alignments:

	Score (bits)	E Value
<u>gi 1438904 gb AAC50623.1 </u> 5-HT4L receptor > <u>gi 2494993 sp Q1...</u>	410	e-113 G
<u>gi 32481997 gb AAP84351.1 </u> neuropeptide Y receptor Y5 [Homo...]	389	e-107 G
<u>gi 11875770 gb AAG40773.1 </u> neuropeptide Y receptor Y5 [Maca...]	389	e-107
<u>gi 14029710 gb AAK52800.1 </u> NPY receptor 5 [Cavia porcellus]	380	e-104
<u>gi 50978824 ref NP_001003118.1 </u> neuropeptide Y receptor typ...	379	e-104 G
<u>gi 1438906 gb AAC52677.1 </u> 5-HT4L receptor > <u>gi 2494994 sp Q6...</u>	364	2e-99 G
<u>gi 4249729 gb AAD13778.1 </u> neuropeptide Y5 receptor [Sus scr...]	360	3e-98
<u>gi 6981284 ref NP_037001.1 </u> neuropeptide Y receptor Y5; Neu...	360	3e-98 G
<u>gi 2564651 gb AAB81829.1 </u> neuropeptide Y Y5 receptor [Mus m...]	350	3e-95 G
<u>gi 7710072 ref NP_057917.1 </u> neuropeptide Y receptor Y5 [Mus...]	350	3e-95 G
<u>gi 3169285 gb AAC17839.1 </u> neuropeptide Y receptor type 5 [M...]	348	1e-94 G
<u>gi 50746172 ref XP_420388.1 </u> PREDICTED: similar to neuropep...	281	2e-74 G
<u>gi 19548984 gb AAK83556.1 </u> neuropeptide Y receptor Y5 [Gall...]	271	3e-71
<u>gi 33302263 gb AAO62565.1 </u> NPY receptor Y1 [Squalus acanthias]	116	5e-57
<u>gi 19548986 gb AAK83557.1 </u> neuropeptide Y receptor Y1 [Gall...]	118	3e-55
<u>gi 33302259 gb AAO62564.1 </u> NPY receptor Y6 [Squalus acanthias]	108	2e-53
<u>gi 2134119 pir  S71152</u> neuropeptide Y/peptide YY receptor Y...	114	3e-53 G
<u>gi 50746252 ref XP_426285.1 </u> PREDICTED: similar to neuropep...	118	5e-53 G
<u>gi 47523648 ref NP_999453.1 </u> neuropeptide Y Y1 receptor [Su...]	118	5e-52 G

<a href="#">gi 6457648 gb AAD13776.2 </a>	neuropeptide Y1 receptor [Sus scrofa]	118	5e-52	G
<a href="#">gi 18859127 ref NP_571515.1 </a>	neuropeptide Y/peptide YY receptor	124	9e-52	G
<a href="#">gi 50950123 ref NP_001002930.1 </a>	neuropeptide Y receptor Y1 [Homosapiens]	116	3e-51	G
<a href="#">gi 4505445 ref NP_000900.1 </a>	neuropeptide Y receptor Y1 [Homosapiens]	114	1e-50	G
<a href="#">gi 11875766 gb AAG40771.1 </a>	neuropeptide Y receptor Y1 [Macaca fasciata]	114	1e-50	
<a href="#">gi 5410446 gb AAD43060.1 </a>	neuropeptide Y receptor Y1 [Cavia porcellus]	115	2e-50	
<a href="#">gi 34877858 ref XP_344503.1 </a>	neuropeptide Y receptor Y1 [Rattus norvegicus]	116	4e-50	G
<a href="#">gi 189154 gb AAA59920.1 </a>	neuropeptide Y receptor	112	6e-50	G
<a href="#">gi 57637 emb CAA77579.1 </a>	NPY-1 receptor [Rattus rattus] >gi 57637 emb CAA77579.1	115	8e-50	G
<a href="#">gi 111640 pir S12863 </a>	G protein-coupled receptor FC5 - rat	115	8e-50	
<a href="#">gi 30410856 gb AAH51420.1 </a>	Npylr protein [Mus musculus] >gi 30410856 gb AAH51420.1	114	1e-49	G
<a href="#">gi 4106397 gb AAD02833.1 </a>	neuropeptide Y/peptide YY receptor	102	1e-45	
<a href="#">gi 6754884 ref NP_035065.1 </a>	neuropeptide Y receptor Y6 [Mus musculus]	105	1e-45	G
<a href="#">gi 18253297 gb AAL66410.1 </a>	NPY receptor [Lampetra fluviatilis]	118	3e-44	
<a href="#">gi 33302257 gb AAO62563.1 </a>	NPY receptor Y4 [Squalus acanthias]	114	2e-43	
<a href="#">gi 19071213 gb AAL84161.1 </a>	neuropeptide Y receptor 4 [Gallus gallus]	108	5e-43	
<a href="#">gi 37778942 gb AAN78328.1 </a>	neuropeptide Y receptor Y6 [Pecari tajacu]	100	2e-42	
<a href="#">gi 50746142 ref XP_420373.1 </a>	PREDICTED: similar to neuropeptide Y receptor	112	3e-40	G
<a href="#">gi 11545537 gb AAG37898.1 </a>	neuropeptide Y receptor Y2 [Gallus gallus]	112	3e-40	
<a href="#">gi 49456855 emb CAG46748.1 </a>	PPYR1 [Homo sapiens]	113	5e-40	G
<a href="#">gi 46410163 gb AAS93941.1 </a>	NPY receptor Y7 [Danio rerio]	112	5e-40	
<a href="#">gi 50749562 ref XP_426511.1 </a>	PREDICTED: similar to neuropeptide Y receptor	97	1e-39	G
<a href="#">gi 47217601 emb CAG02528.1 </a>	unnamed protein product [Tetraodon nigroviridis]	94	2e-39	
<a href="#">gi 18859129 ref NP_571511.1 </a>	neuropeptide Y/peptide YY receptor	105	3e-39	G
<a href="#">gi 7417238 gb AAF62507.1 </a>	neuropeptide Y-family receptor Y4 [Danio rerio]	111	4e-39	G
<a href="#">gi 4235257 gb AAD13143.1 </a>	neuropeptide Y receptor type 2 [Ciona intestinalis]	111	5e-39	
<a href="#">gi 51452114 gb AAH75053.2 </a>	Neuropeptide Y receptor Y2 [Homo sapiens]	111	7e-39	G
<a href="#">gi 961480 dbj BAA09888.1 </a>	neuropeptide Y-Y1beta receptor [Mus musculus]	114	7e-39	G
<a href="#">gi 1314330 gb AAB07760.1 </a>	neuropeptide Y/peptide YY receptor	110	1e-38	G
<a href="#">gi 6679122 ref NP_032757.1 </a>	neuropeptide Y receptor Y2; NPY receptor	111	1e-38	G
<a href="#">gi 26340626 dbj BAC33975.1 </a>	unnamed protein product [Mus musculus]	111	1e-38	G
<a href="#">gi 50755049 ref XP_414599.1 </a>	PREDICTED: similar to NPY receptor	117	2e-38	G
<a href="#">gi 13027422 ref NP_076458.1 </a>	neuropeptide Y receptor Y2; neuropeptide Y receptor	110	2e-38	G
<a href="#">gi 1000751 gb AAA93170.1 </a>	type 2 neuropeptide Y receptor	109	2e-38	G
<a href="#">gi 4249727 gb AAD13777.1 </a>	neuropeptide Y2 receptor [Sus scrofa]	112	3e-38	
<a href="#">gi 27806023 ref NP_776826.1 </a>	neuropeptide Y receptor Y2 [Boophis tephrosceles]	110	3e-38	G
<a href="#">gi 13928788 ref NP_113769.1 </a>	pancreatic polypeptide receptor	112	3e-38	G
<a href="#">gi 1109769 emb CAA92322.1 </a>	pancreatic polypeptide receptor	112	3e-38	G
<a href="#">gi 47523392 ref NP_999315.1 </a>	neuropeptide Y Y2 receptor [Sus scrofa]	111	3e-38	G
<a href="#">gi 11875768 gb AAG40772.1 </a>	neuropeptide Y receptor Y2 [Macaca fasciata]	110	4e-38	
<a href="#">gi 4098212 gb AAD00248.1 </a>	neuropeptide Y receptor type 2 [Homo sapiens]	111	1e-37	G
<a href="#">gi 4235259 gb AAD13144.1 </a>	pancreatic polypeptide receptor Y2	105	2e-37	
<a href="#">gi 18859131 ref NP_571512.1 </a>	neuropeptide Y/peptide YY receptor	105	6e-37	G
<a href="#">gi 47228590 emb CAG05410.1 </a>	unnamed protein product [Tetraodon nigroviridis]	100	5e-36	
<a href="#">gi 4758474 ref NP_004239.1 </a>	G protein-coupled receptor 10; neuropeptide Y receptor	100	2e-35	G
<a href="#">gi 31239533 ref XP_320180.1 </a>	ENSANGP00000011806 [Anopheles gambiae]	98	4e-35	G
<a href="#">gi 47223673 emb CAF99282.1 </a>	unnamed protein product [Tetraodon nigroviridis]	92	2e-34	
<a href="#">gi 1002739 gb AAC50504.1 </a>	GPR10	94	3e-33	G
<a href="#">gi 50749931 ref XP_426542.1 </a>	PREDICTED: similar to Prolactin receptor	92	8e-33	G

<u>gi 47228890 emb CAG09405.1 </u>	unnamed protein product [Tetrao...	<u>110</u>	<u>1e-32</u>	
<u>gi 31208067 ref XP_313000.1 </u>	ENSANGP00000020441 [Anopheles ...	<u>88</u>	<u>2e-30</u>	
<u>gi 17945440 gb AAL48774.1 </u>	RE18294p [Drosophila melanogaster]	<u>91</u>	<u>8e-30</u>	
<u>gi 28571531 ref NP_524245.3 </u>	CG1147-PA [Drosophila melanoga...	<u>91</u>	<u>8e-30</u>	
<u>gi 13937102 gb AAK50050.1 </u>	neuropeptide F receptor [Drosoph...	<u>91</u>	<u>8e-30</u>	
<u>gi 38087207 ref XP_142008.2 </u>	similar to G protein-coupled r...	<u>105</u>	<u>1e-29</u>	
<u>gi 34880717 ref XP_231463.2 </u>	similar to G protein-coupled r...	<u>106</u>	<u>3e-29</u>	
<u>gi 50745619 ref XP_426254.1 </u>	PREDICTED: similar to G protei...	<u>93</u>	<u>1e-28</u>	
<u>gi 1679632 gb AAB19187.1 </u>	truncated pancreatic polypeptide ...	<u>100</u>	<u>2e-28</u>	
<u>gi 50731261 ref XP_425651.1 </u>	PREDICTED: similar to G protei...	<u>96</u>	<u>2e-28</u>	
<u>gi 1731790 dbj BAA13103.1 </u>	Y6 encoding protein [Homo sapiens]	<u>100</u>	<u>4e-28</u>	
<u>gi 1857635 gb AAD11810.1 </u>	lymkinin receptor [Lymnaea stag...	<u>97</u>	<u>2e-27</u>	
<u>gi 5420385 emb CAA57620.1 </u>	G protein-coupled receptor 105 [...]	<u>83</u>	<u>4e-27</u>	
<u>gi 85080 pir  A41738</u>	neuropeptide Y receptor - fruit fly (D...	<u>94</u>	<u>4e-27</u>	
<u>gi 24643096 ref NP_523404.2 </u>	CG6857-PA [Drosophila melanoga...	<u>106</u>	<u>7e-27</u>	
<u>gi 51092236 gb AAT94531.1 </u>	AT16733p [Drosophila melanogaster]	<u>93</u>	<u>7e-27</u>	
<u>gi 45549233 ref NP_524525.3 </u>	CG5811-PA [Drosophila melanoga...	<u>93</u>	<u>7e-27</u>	
<u>gi 25152230 ref NP_509725.2 </u>	neuropeptide receptor NPR1 (46...	<u>77</u>	<u>7e-27</u>	
<u>gi 7959347 dbj BAA96064.1 </u>	KIAA1540 protein [Homo sapiens]	<u>97</u>	<u>2e-26</u>	
<u>gi 45768492 gb AAH67473.1 </u>	G protein-coupled receptor 83 [H...	<u>97</u>	<u>2e-26</u>	
<u>gi 33354257 ref NP_057624.2 </u>	G protein-coupled receptor 83;...	<u>97</u>	<u>2e-26</u>	
<u>gi 7248882 gb AAF43705.1 </u>	orphan G-protein coupled receptor...	<u>97</u>	<u>2e-26</u>	
<u>gi 50978808 ref NP_001003108.1 </u>	glucocorticoid induced rece...	<u>97</u>	<u>2e-26</u>	
<u>gi 34860282 ref XP_346816.1 </u>	hypothetical protein XP_346815...	<u>96</u>	<u>6e-26</u>	
<u>gi 14028711 gb AAK52473.1 </u>	allatostatin receptor [Periplane...	<u>88</u>	<u>8e-26</u>	
<u>gi 25388079 pir  JC7677</u>	allatostatin receptor - American co...	<u>88</u>	<u>8e-26</u>	
<u>gi 2707338 gb AAB92258.1 </u>	cardioexcitatory receptor [Lymnae...	<u>78</u>	<u>8e-26</u>	
<u>gi 45767703 gb AAH67474.1 </u>	G protein-coupled receptor 83 [H...	<u>94</u>	<u>1e-25</u>	
<u>gi 48139558 ref XP_397024.1 </u>	similar to allatostatin recept...	<u>93</u>	<u>1e-25</u>	
<u>gi 14279167 gb AAK58514.1 </u>	G-protein-coupled receptor 74 [M...	<u>96</u>	<u>1e-25</u>	
<u>gi 6753988 ref NP_034417.1 </u>	G protein-coupled receptor 83; ...	<u>94</u>	<u>1e-25</u>	
<u>gi 45383432 ref NP_989693.1 </u>	neuropeptide FF 1, RFamide-rel...	<u>98</u>	<u>1e-25</u>	

**Alignments**

Get selected sequences     Select all     Deselect all

>gi|1438904|gb|AAC50623.1| 5-HT4L receptor  
gi|2494993|sp|Q15761|NY5R\_HUMAN Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (NPYY5)  
Length = 455

Score = 410 bits (1054), Expect = e-113  
Identities = 212/263 (80%), Positives = 227/263 (86%), Gaps = 7/263 (2%)  
Frame = +2

Query: 17 MSFYSKQDYNMDLELDEYYNKTTLATEENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF 196  
MSFYSKQDYNMDLELDEYYNKTTLATEENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF  
Sbjct: 1 MSFYSKQDYNMDLELDEYYNKTTLATEENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF 60

RID=1098302862-16212-154863854574.BLASTQ4,

Query: 197 VSLLGFMGNLLILMALKRNRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFG 376  
VSLLGFMGNLLILMALKRNRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFG  
Sbjct: 61 VSLLGFMGNLLILMALKRNRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFG 120

Query: 377 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATWVTLGFAI 556  
KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATWVTLGFAI  
Sbjct: 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATWVTLGFAI 180

Query: 557 CSPLPVFHSLVELQETFGSALLAAGIYVL---SHGHЛИTELPLLСLYC\*FSYSALSLS 724  
CSPLPVFHSLVELQETFGSALL++ + S + I + LL + L++S  
Sbjct: 181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVS 240

Query: 725 Y---CKSYKCLHTPKKEKQHDGQ 784  
+ C+S C + K+ + +  
Sbjct: 241 HTSVCRSISCGLSNKENRLEENE 263

Score = 172 bits (437), Expect = 1e-41  
Identities = 80/80 (100%), Positives = 80/80 (100%)  
Frame = +3

Query: 825 VFYRLTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 1004  
VFYRLTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY  
Sbjct: 376 VFYRLTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 435

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064  
GFLNNGIKADLVSLIHCLHM  
Sbjct: 436 GFLNNGIKADLVSLIHCLHM 455

Score = 60.5 bits (145), Expect(2) = 2e-12  
Identities = 28/34 (82%), Positives = 30/34 (88%)  
Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQQLFCP 714  
++ SSRYLCVESWPSDSYRIAFTISLLLQ P  
Sbjct: 200 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 233

Score = 35.0 bits (79), Expect(2) = 2e-12  
Identities = 15/15 (100%), Positives = 15/15 (100%)  
Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749  
ILPLVCLTVSHTSVC  
Sbjct: 231 ILPLVCLTVSHTSVC 245

□>gi|32481997|gb|AAP84351.1| G neuropeptide Y receptor Y5 [Homo sapiens]  
gi|5453796|ref|NP\_006165.1| G neuropeptide Y receptor Y5 [Homo sapiens]  
gi|27502796|gb|AAH42416.1| G Neuropeptide Y receptor Y5 [Homo sapiens]  
gi|1945449|gb|AAC51295.1| G neuropeptide Y5 receptor [Homo sapiens]  
gi|1620656|gb|AAC50741.1| G neuropeptide Y5 receptor  
Length = 445

Score = 389 bits (999), Expect = e-107  
 Identities = 202/253 (79%), Positives = 217/253 (85%), Gaps = 7/253 (2%)  
 Frame = +2

Query: 47 MDLELDEYYNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226  
 MDLELDEYYNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL

Sbjct: 1 MDLELDEYYNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL 406  
 LILMALKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL

Sbjct: 61 LILMALKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATWTLGFAICSLPVFHSL 586  
 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATWTLGFAICSLPVFHSL

Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATWTLGFAICSLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL---SHGHЛИHTELPLLSLYC\*FSYSALSLSY---CKSYKC 745  
 VELQETFGSALL++ + S + I + LL + L++S+ C+S C

Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784

+ K+ + + +

Sbjct: 241 GLSNKENRLEENE 253

Score = 172 bits (437), Expect = 1e-41  
 Identities = 80/80 (100%), Positives = 80/80 (100%)  
 Frame = +3

Query: 825 VFYRLTILILVFAWSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 1004  
 VFYRLTILILVFAWSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY

Sbjct: 366 VFYRLTILILVFAWSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064

GFLNNGIKADLVSLIHCLHM

Sbjct: 426 GFLNNGIKADLVSLIHCLHM 445

Score = 60.5 bits (145), Expect(2) = 2e-12  
 Identities = 28/34 (82%), Positives = 30/34 (88%)  
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQQLFCP 714

++ SSRYLCVESWPSDSYRIAFTISLLLQ P

Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 223

Score = 35.0 bits (79), Expect(2) = 2e-12  
 Identities = 15/15 (100%), Positives = 15/15 (100%)  
 Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749

ILPLVCLTVSHTSVC

Sbjct: 221 ILPLVCLTVSHTSVC 235

>gi|11875770|gb|AAG40773.1| neuropeptide Y receptor Y5 [Macaca mulatta]  
Length = 445

Score = 389 bits (999), Expect = e-107  
Identities = 202/253 (79%), Positives = 217/253 (85%), Gaps = 7/253 (2%)  
Frame = +2

Query: 47 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226  
MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL  
Sbjct: 1 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKRNQKTTVNFLIGNLAFLSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL 406  
LILMALMKRNQKTTVNFLIGNLAFLSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL  
Sbjct: 61 LILMALMKRNQKTTVNFLIGNLAFLSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586  
QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL  
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL---SHGHЛИHTELPLLSLYC\*FSYSALSLSY---CKSYKC 745  
VELQETFGSALL++ + S + I + LL + L++S+ C+S C  
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784  
+ K+ + + +  
Sbjct: 241 GLSNKENRLEENE 253

Score = 171 bits (434), Expect = 2e-41  
Identities = 79/80 (98%), Positives = 80/80 (100%)  
Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004  
VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY  
Sbjct: 366 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHLHM 1064  
GFLNNGIKADL+SLIHLHM  
Sbjct: 426 GFLNNGIKADLMSLIHLHM 445

Score = 60.5 bits (145), Expect(2) = 2e-12  
Identities = 28/34 (82%), Positives = 30/34 (88%)  
Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQLFCP 714  
++ SSRYLCVESWPSDSYRIAFTISLLLQ P  
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 223

Score = 35.0 bits (79), Expect(2) = 2e-12  
Identities = 15/15 (100%), Positives = 15/15 (100%)  
Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749  
ILPLVCLTVSHTSVC

RID=1098302862-16212-154863854574.BLASTQ4,

Sbjct: 221 ILPLVCLTVSHTSVC 235

>gi|14029710|gb|AAK52800.1| NPY receptor 5 [Cavia porcellus]  
Length = 446

Score = 380 bits (977), Expect = e-104  
Identities = 197/253 (77%), Positives = 214/253 (84%), Gaps = 7/253 (2%)  
Frame = +2

Query: 47 MDLELDEYYNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226  
MDLEL EYYNKTLENNT TRNSDFPVWDDY+SSVDDLQYFLIGLYTFVSLLGFMGNL  
Sbjct: 1 MDLELKEYYNKTLENNTTTRNSDFPVWDDYRSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFAFSIDL VVLFCSPTLTSVLLDQWMFGKVMCHIMPFL 406  
LILMAL+KKRNQKTTVNFLIGNLAFAFSIDL VVLFCSPTLTSVLLDQWMFGKVMCHIMPFL  
Sbjct: 61 LILMALIKKRNQKTTVNFLIGNLAFAFSIDL VVLFCSPTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586  
QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL  
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL---SHGHLIHTELPLLSLYC\*FSYSALSLSY---CKSYKC 745  
VELQETFGSALL++ + S + I + LL + L++S+ C+S C  
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784  
+ K+ + + +  
Sbjct: 241 GLSNKENRLEENE 253

Score = 170 bits (431), Expect = 5e-41  
Identities = 78/80 (97%), Positives = 80/80 (100%)  
Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004  
VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY  
Sbjct: 366 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064  
GFLNNGIKADL+SLIHCLH+  
Sbjct: 426 GFLNNGIKADLMSLIHCLHL 445

Score = 60.5 bits (145), Expect(2) = 2e-12  
Identities = 28/34 (82%), Positives = 30/34 (88%)  
Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQLFCP 714  
++ SSRYLCVESWPSDSYRIAFTISLLLQ P  
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 223

Score = 35.0 bits (79), Expect(2) = 2e-12  
Identities = 15/15 (100%), Positives = 15/15 (100%)  
Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749  
 ILPLVCLTVSHTSVC  
 Sbjct: 221 ILPLVCLTVSHTSVC 235

□>gi|50978824|ref|NP\_001003118.1| G neuropeptide Y receptor type 5 [Canis familiaris]  
 gi|3169283|gb|AAC17838.1| G neuropeptide Y receptor type 5 [Canis familiaris]  
 gi|3914178|sp|O62729|NY5R CANFA Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (NPYY5)  
 Length = 446

Score = 379 bits (973), Expect = e-104  
 Identities = 197/253 (77%), Positives = 214/253 (84%), Gaps = 7/253 (2%)  
 Frame = +2

Query: 47 MDLELDEYYNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226  
 MDLEL ++YNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL  
 Sbjct: 1 MDLELQDFYNKTLENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL 406  
 LILMALM+KRNQKT VNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL  
 Sbjct: 61 LILMALMRKRNQKTMVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586  
 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL  
 Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL---SHGHLIHTELPLLSLYC\*FSYSALSLSY---CKSYKC 745  
 VELQETF SALL++ + S + I + LL + L++S+ C+S C  
 Sbjct: 181 VELQETFDSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784  
 + K+ K + +  
 Sbjct: 241 GLSNKENKLEENE 253

Score = 169 bits (428), Expect = 1e-40  
 Identities = 78/80 (97%), Positives = 79/80 (98%)  
 Frame = +3

Query: 825 VFYRLTILILVFAWSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 1004  
 VFYRLTILILVFAWSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY  
 Sbjct: 366 VFYRLTILILVFAWSWMPHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHLHM 1064  
 GFLNNGIKADL+SLI CLHM  
 Sbjct: 426 GFLNNGIKADLISLIQCLHM 445

Score = 60.5 bits (145), Expect(2) = 1e-12  
 Identities = 28/34 (82%), Positives = 30/34 (88%)  
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQLFCP 714  
 ++ SSRYLCVESWPSDSYRIAFTISLLLQ P

RID=1098302862-16212-154863854574.BLASTQ4,

Subjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 223

Score = 36.2 bits (82), Expect(2) = 1e-12  
Identities = 18/33 (54%), Positives = 24/33 (72%), Gaps = 1/33 (3%)  
Frame = +3

Query: 705 ILPLVCLTVSHTSVCIRLK-RRNNMMDKMRDNK 800

ILPLVCLTVSHTSVC + +N +K+ +N+

Subjct: 221 ILPLVCLTVSHTSVCRSISCGLSNKENKLEENE 253

>gi|1438906|gb|AAC52677.1| G 5-HT4L receptor  
gi|2494994|sp|Q63634|NY5R RAT G Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor)  
Length = 456

Score = 364 bits (934), Expect = 2e-99  
Identities = 186/257 (72%), Positives = 212/257 (82%), Gaps = 7/257 (2%)  
Frame = +2

Query: 35 QDYNMDLELDEYYNKTIATEENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGF 214  
QD +M+ +L+E++NKT TENNTAA RN+ FP W+DY+ SVDDLQYFLIGLYTFVSLLGF

Subjct: 8 QDSSMEFKLEEHFNKTFTVTEENNTAAARNAAFPAWEDYRGSVDDLQYFLIGLYTFVSLLGF 67

Query: 215 MGNLLILMALKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKVMCHI 394  
MGNLLILMA+MKKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGK MCHI

Subjct: 68 MGNLLILMAVMKKRNQKTTVNFLIGNLAFSDILVVLCSPFTLTSVLLDQWMFGKAMCHI 127

Query: 395 MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV 574  
MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV

Subjct: 128 MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV 187

Query: 575 FHSLVELQETFGSALLAAGIYVL---SHGHLIHTELPLLSLYC\*FSYSALSLSY---CK 733  
FHSLVEL+ETFGSALL++ + S + I + LL + L++S+ C+

Subjct: 188 FHSLVELKETFGSALLSKYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVC 247

Query: 734 SYKCLHTPKKEKQHDGQ 784

S C + K+ + +

Subjct: 248 SISCGLSHKENRLEENE 264

Score = 167 bits (424), Expect = 3e-40  
Identities = 77/80 (96%), Positives = 79/80 (98%)  
Frame = +3

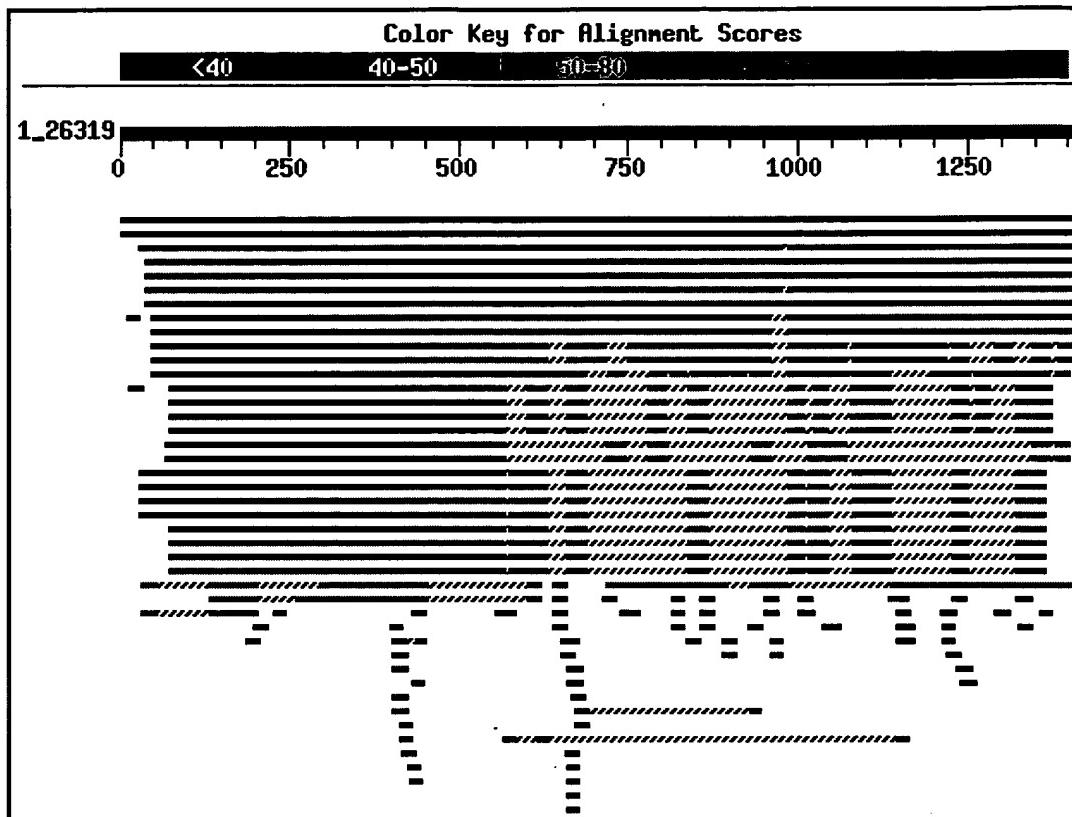
Query: 825 VFYRLTILILVFAWSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 1004  
VFYRLTILILVFAWSWMPLH+HVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY

Subjct: 376 VFYRLTILILVFAWSWMPLHVFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCLNPILY 435

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064

GFLNNGIKADL +LIHCLHM

Subjct: 436 GFLNNGIKADLRALIHCLHM 455



Sequences producing significant alignments:

		Score (bits)	E Value
--	--	-----------------	------------

<u>gi 16756377 gb AC079238.7 </u>	Homo sapiens BAC clone RP11-719L...	<u>1132</u>	0.0	G U
<u>gi 1438903 gb U56079.1 HSU56079</u>	Human Y5 receptor mRNA, com...	<u>1132</u>	0.0	G U
<u>gi 1620655 gb U66275.1 HSU66275</u>	Human neuropeptide Y5 recep...	<u>1074</u>	0.0	G U
<u>gi 22832895 gb BC034224.1 </u>	Homo sapiens neuropeptide Y rece...	<u>1059</u>	0.0	G U
<u>gi 31377784 ref NM_006174.2 </u>	Homo sapiens neuropeptide Y re...	<u>1059</u>	0.0	G U E
<u>gi 27502795 gb BC042416.1 </u>	Homo sapiens neuropeptide Y rece...	<u>1059</u>	0.0	G U
<u>gi 1945448 gb U94320.1 HSU94320</u>	Human neuropeptide Y5 recep...	<u>1059</u>	0.0	G U E
<u>gi 32481996 gb AY322538.1 </u>	Homo sapiens neuropeptide Y rece...	<u>1041</u>	0.0	G
<u>gi 11875769 gb AF303091.1 AF303091</u>	Macaca mulatta neuropept...	<u>969</u>	0.0	
<u>gi 50978823 ref NM_001003118.1 </u>	Canis familiaris neuropepti...	<u>779</u>	0.0	G U
<u>gi 3169282 gb AF049328.1 AF049328</u>	Canis familiaris neuropep...	<u>779</u>	0.0	G U E
<u>gi 14029709 gb AF363240.1 AF363240</u>	Cavia porcellus NPY rece...	<u>660</u>	0.0	
<u>gi 6981283 ref NM_012869.1 </u>	Rattus norvegicus neuropeptide ...	<u>545</u>	e-152	G U E
<u>gi 1620657 gb U66274.1 RNU66274</u>	Rattus norvegicus neuropept...	<u>545</u>	e-152	G U E
<u>gi 1438905 gb U56078.1 RNU56078</u>	Rattus norvegicus Y5 recept...	<u>545</u>	e-152	G U
<u>gi 3098509 gb AF044264.1 AF044264</u>	Rattus norvegicus neurope...	<u>545</u>	e-152	G U
<u>gi 4249728 gb AF106083.1 AF106083</u>	Sus scrofa neuropeptide Y...	<u>539</u>	e-150	
<u>gi 3808059 dbj AB019185.1 </u>	Sus scrofa NPY Y5 gene for neuro...	<u>539</u>	e-150	
<u>gi 22476189 gb AC123796.2 </u>	Mus musculus BAC clone RP24-320P...	<u>523</u>	e-145	
<u>gi 33942177 gb AC116731.9 </u>	Mus musculus chromosome 8, clone...	<u>523</u>	e-145	
<u>gi 52839799 gb AC100541.17 </u>	Mus musculus chromosome 8, clon...	<u>523</u>	e-145	
<u>gi 2564650 gb AF022948.1 AF022948</u>	Mus musculus neuropeptide...	<u>523</u>	e-145	G

<u>gi 26337480 dbj AK045587.1 </u>	Mus musculus adult male corpora...	523	e-145	G U
<u>gi 3169284 gb AF049329.1 AF049329</u>	Mus musculus neuropeptide...	519	e-144	G U E
<u>gi 7710071 ref NM_016708.1 </u>	Mus musculus neuropeptide Y rec...	515	e-143	G U E
<u>gi 6714644 dbj AB001346.1 </u>	Mus musculus mRNA for neuropepti...	515	e-143	G U E
<u>gi 50746171 ref XM_420388.1 </u>	PREDICTED: Gallus gallus simil...	98	7e-17	G
<u>gi 19548983 gb AY040844.1 </u>	Gallus gallus neuropeptide Y rec...	92	4e-15	
<u>gi 976208 gb L47169.1 HUMNPYAC</u>	Homo sapiens neuropeptide Y ...	70	2e-08	
<u>gi 46427829 emb CR389184.1 </u>	Gallus gallus finished cDNA, cl...	56	2e-04	U
<u>gi 51100952 dbj AB104827.2 </u>	Candida boidinii FGH1 gene for ...	44	0.87	
<u>gi 31746714 gb AC133101.4 </u>	Mus musculus BAC clone RP23-154M...	42	3.5	
<u>gi 37693674 gb AC121082.13 </u>	Mus musculus chromosome 7, clon...	42	3.5	
<u>gi 32880270 gb AC118695.10 </u>	Mus musculus chromosome 19, clo...	42	3.5	
<u>gi 53379715 gb AC149588.4 </u>	Mus musculus chromosome 15 clone...	42	3.5	
<u>gi 52077841 gb AC132394.3 </u>	Mus musculus chromosome 6 clone ...	42	3.5	
<u>gi 16603965 gb AC076968.38 </u>	Homo sapiens 12 BAC RP11-686F15...	42	3.5	
<u>gi 48675465 gb AC132104.3 </u>	Mus musculus BAC clone RP24-364N...	42	3.5	
<u>gi 34536220 dbj AK128706.1 </u>	Homo sapiens cDNA FLJ46873 fis,...	42	3.5	U
<u>gi 49170190 gb AC124958.13 </u>	Medicago truncatula clone mth2-...	42	3.5	
<u>gi 21955079 gb AC104016.8 </u>	Homo sapiens chromosome 11, clon...	42	3.5	
<u>gi 20334476 gb AC079822.13 </u>	Homo sapiens 3 BAC RP11-413G22 ...	42	3.5	
<u>gi 22549646 gb AC092964.8 </u>	Homo sapiens 3 BAC RP11-423E7 (R...	42	3.5	
<u>gi 20986479 gb AC084701.5 </u>	Homo sapiens chromosome 18, clon...	42	3.5	
<u>gi 2462139 emb Z70681.1 CEC30F2</u>	Caenorhabditis elegans cosm...	42	3.5	
<u>gi 28173126 gb AC100865.5 </u>	Homo sapiens chromosome 11, clon...	42	3.5	
<u>gi 27884981 gb AC117539.6 </u>	Papio hamadryas, clone RP41-208E...	42	3.5	
<u>gi 15638824 gb AC096569.1 </u>	Homo sapiens BAC clone RP11-347B...	42	3.5	
<u>gi 14702085 gb AC013722.8 </u>	Homo sapiens BAC clone RP11-299H...	42	3.5	
<u>gi 15431133 gb AC013660.9 </u>	Homo sapiens, clone RP11-20A14, ...	42	3.5	
<u>gi 2109298 gb AF000132.1 AHAF000132</u>	Amaranthus hypochondria...	42	3.5	
<u>gi 13560010 emb AL356318.7 </u>	Human DNA sequence from clone R...	42	3.5	
<u>gi 24366576 emb AL808118.8 </u>	Mouse DNA sequence from clone R...	42	3.5	
<u>gi 10280826 gb AC012531.11 AC012531</u>	Homo sapiens, clone RP1...	42	3.5	
<u>gi 42491502 gb AC102734.11 </u>	Mus musculus chromosome 6, clon...	42	3.5	
<u>gi 608510 gb U16311.1 BRU16311</u>	Brachydanio rerio homeodomai...	42	3.5	G U
<u>gi 26330583 dbj AK035302.1 </u>	Mus musculus adult male urinary...	42	3.5	G U
<u>gi 26084230 dbj AK034836.1 </u>	Mus musculus 12 days embryo emb...	42	3.5	G U
<u>gi 21211711 emb AL359771.27 </u>	Human DNA sequence from clone ...	42	3.5	
<u>gi 38678612 gb AC117702.10 </u>	Mus musculus chromosome 10, clo...	40	14	
<u>gi 17570664 ref NM_077495.1 </u>	Caenorhabditis elegans allatos...	40	14	G
<u>gi 28604212 gb AC124775.4 </u>	Mus musculus BAC clone RP23-60N3...	40	14	
<u>gi 19310330 gb AC104789.4 </u>	Homo sapiens BAC clone RP11-138B...	40	14	
<u>gi 48391178 gb AY584422.1 </u>	Xantisia bezyi isolate Xbe5_Pin5...	40	14	
<u>gi 48391102 gb AY584384.1 </u>	Xantisia bezyi isolate Xbe2_GaL1...	40	14	
<u>gi 34368596 gb AC120736.4 </u>	Rattus norvegicus 11 BAC CH230-2...	40	14	
<u>gi 33242564 gb AY336522.1 </u>	Sulfolobus solfataricus strain P...	40	14	
<u>gi 44844336 emb BX247953.2 </u>	Mouse DNA sequence from clone R...	40	14	
<u>gi 30725969 gb AC100271.6 </u>	Mus musculus, clone RP23-77E14, ...	40	14	
<u>gi 51233561 gb AC110499.19 </u>	Mus musculus chromosome 1, clon...	40	14	
<u>gi 51036712 gb AC130808.26 </u>	Medicago truncatula clone mth2-...	40	14	
<u>gi 50761406 ref XM_424720.1 </u>	PREDICTED: Gallus gallus simil...	40	14	G
<u>gi 20258986 gb AY091270.1 </u>	Arabidopsis thaliana putative si...	40	14	G U
<u>gi 17380917 gb AY063915.1 </u>	Arabidopsis thaliana putative pu...	40	14	G U
<u>gi 48675548 gb AC134472.4 </u>	Mus musculus BAC clone RP23-123E...	40	14	
<u>gi 46195482 gb AC135316.15 </u>	Medicago truncatula clone mth2-...	40	14	
<u>gi 22539131 gb AC105009.13 </u>	Homo sapiens chromosome 8, clon...	40	14	

<u>gi 21909528 gb AC105235.7 </u>	Homo sapiens chromosome 8, clone...	40	14
<u>gi 34786898 emb AL831812.5 CNS08CAP</u>	Oryza sativa chromosome...	40	14
<u>gi 21535755 emb AL713907.3 CNS07YQ7</u>	Oryza sativa chromosome...	40	14
<u>gi 10944453 gb AC008752.6 </u>	Homo sapiens chromosome 19 clone...	40	14
<u>gi 33620400 emb AL929018.14 </u>	Mouse DNA sequence from clone ...	40	14
<u>gi 21281541 gb AC104163.2 </u>	Homo sapiens chromosome 3 clone ...	40	14
<u>gi 48717527 gb AC122169.23 </u>	Medicago truncatula clone mth2-...	40	14
<u>gi 27228874 gb AC093576.3 </u>	Homo sapiens chromosome 1 clone ...	40	14
<u>gi 49528096 emb CR380958.1 </u>	Candida glabrata strain CBS138 ...	40	14
<u>gi 25137544 dbj AP005900.1 </u>	Homo sapiens genomic DNA, chrom...	40	14
<u>gi 17921243 gb AC022317.8 </u>	Homo sapiens chromosome 4 clone ...	40	14
<u>gi 17985904 gb AC093581.2 </u>	Homo sapiens chromosome 1 clone ...	40	14
<u>gi 17155036 gb AC091819.3 </u>	Homo sapiens chromosome 5 clone ...	40	14
<u>gi 24417223 dbj AP005663.2 </u>	Homo sapiens genomic DNA, chrom...	40	14
<u>gi 13992802 gb AC068551.6 </u>	Homo sapiens BAC clone RP11-720N...	40	14
<u>gi 16554344 gb AC011395.5 </u>	Homo sapiens chromosome 5 clone ...	40	14
<u>gi 46240964 gb AC145942.4 </u>	Gallus gallus chromosome UNK clo...	40	14
<u>gi 11968293 gb AC010368.4 AC010368</u>	Homo sapiens chromosome ...	40	14
<u>gi 47847914 dbj AP004168.3 </u>	Oryza sativa (japonica cultivar...	40	14
<u>gi 12309635 emb AL450428.6 </u>	Human DNA sequence from clone R...	40	14
<u>gi 10441989 gb AF218030.1 AF218030</u>	Homo sapiens clone PP79 ...	40	14 G U
<u>gi 10441953 gb AF218012.1 AF218012</u>	Homo sapiens clone PP379...	40	14 G U E
<u>gi 21734414 emb AL833764.1 HSM805077</u>	Homo sapiens mRNA; cDN...	40	14 G

**Alignments**

>gi|16756377|gb|AC079238.7|    **D** Homo sapiens BAC clone RP11-719L21 from 4, complet  
Length = 142462

Score = 1132 bits (571), Expect = 0.0  
 Identities = 571/571 (100%)  
 Strand = Plus / Plus

Query: 1        ttttggttgctgacaaatgtcttttattccaaggcaggactataatatggatttagagct 60  
                  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 128642 ttttggttgctgacaaatgtcttttattccaaggcaggactataatatggatttagagct 128701

Query: 61        cgacgagtattataacaagacacttgccacagagaataactgctgccactcggaattc 120  
                  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 128702 cgacgagtattataacaagacacttgccacagagaataactgctgccactcggaattc 128761

Query: 121       tgatttcccagtctggatgactataaaaggcagtgttagatgacttacagtatttctgat 180  
                  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 128762 tgatttcccagtctggatgactataaaaggcagtgttagatgacttacagtatttctgat 128821

Query: 181 .      tgggctctatacatgttaagtcttcttgcttatgggaatctacttatttaatggc 240  
                  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 128822 tgggctctatacatgttaagtcttcttgcttatgggaatctacttatttaatggc 128881

Query: 241 tctcataaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300  
 |||||||  
 Sbjct: 128882 tctcataaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 128941

Query: 301 ttctgatatcttgggtgtgtttgctcaccttcacactgacgtctgtcttgta 360  
 |||||||  
 Sbjct: 128942 ttctgatatcttgggtgtgtttgctcaccttcacactgacgtctgtcttgta 129001

Query: 361 tcagtggatgttggcaaagtcatgtgccatattatgcctttcttcaatgtgtcagt 420  
 |||||||  
 Sbjct: 129002 tcagtggatgttggcaaagtcatgtgccatattatgcctttcttcaatgtgtcagt 129061

Query: 421 tttgggttcaacttaatttaatataattcaattgccattgtcaggtatcatatgataaaaca 480  
 |||||||  
 Sbjct: 129062 tttgggttcaacttaatttaatataattcaattgccattgtcaggtatcatatgataaaaca 129121

Query: 481 tccccatatactaataatttaacacgcaaccatggctactttctgatagctactgtctggac 540  
 |||||||  
 Sbjct: 129122 tccccatatactaataatttaacacgcaaccatggctactttctgatagctactgtctggac 129181

Query: 541 actagggtttgccatctgttctccctcca 571  
 |||||||  
 Sbjct: 129182 actagggtttgccatctgttctccctcca 129212

Score = 69.9 bits (35), Expect = 2e-08  
 Identities = 35/35 (100%)  
 Strand = Plus / Plus

Query: 810 cagatgttcatgaattgagagtaaaacgttctgtt 844  
 |||||||  
 Sbjct: 129721 cagatgttcatgaattgagagtaaaacgttctgtt 129755

Score = 65.9 bits (33), Expect = 2e-07  
 Identities = 33/33 (100%)  
 Strand = Plus / Plus

Query: 1254 ttctgttacaagaataaaaaagagatctcgaag 1286  
 |||||||  
 Sbjct: 129749 ttctgttacaagaataaaaaagagatctcgaag 129781

Score = 63.9 bits (32), Expect = 9e-07  
 Identities = 32/32 (100%)  
 Strand = Plus / Plus

Query: 1346 tgatgtcctgttgtttaatccaattctatat 1377

Sbjct: tgatgtcctgttcttaatccaattctatat 129962  
||||||||||||||||||||||||||||||||

Score = 63.9 bits (32), Expect = 9e-07  
Identities = 32/32 (100%)  
Strand = Plus / Plus

Query: 1316 acaatcttatttcaaataaggcatttcaagttg 1347  
|||||||||||||||||||||||||||||||||||  
Sbjct: 129871 acaatcttatttcaaataaggcatttcaagttg 129902

Score = 63.9 bits (32), Expect = 9e-07  
Identities = 32/32 (100%)  
Strand = Plus / Plus

Query: 719 cacagaagaagatatacgaaagaacacgcattg 750  
|||||||||||||||||||||||||||||||||||  
Sbjct: 129540 cacagaagaagatatacgaaagaacacgcattg 129571

Score = 61.9 bits (31), Expect = 4e-06  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 1376 attagtgtcccttatacacactgtcttcata 1406  
|||||||||||||||||||||||||||||||||||  
Sbjct: 129991 attagtgtcccttatacacactgtcttcata 130021

Score = 61.9 bits (31), Expect = 4e-06  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 1287 agtatttgctgttagttggatgccactacac 1317  
|||||||||||||||||||||||||||||||  
Sbjct: 129812 agtatttgctgttagttggatgccactacac 129842

Score = 61.9 bits (31), Expect = 4e-06  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 1226 cttgctttagataaaacctgaagaaaattc 1256  
|||||||||||||||||||||||||||||||  
Sbjct: 129691 cttgctttagataaaacctgaagaaaattc 129721

Score = 61.9 bits (31), Expect = 4e-06  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 1196 actttggctctgtaaaagaagtcagctctcttc 1226  
|||||||  
Sbjct: 129631 actttggctctgtaaaagaagtcagctctcttc 129661

Score = 61.9 bits (31), Expect = 4e-06  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 1107 caacttaactcttcatccatccaaaaagagt 1137  
|||||||  
Sbjct: 129452 caacttaactcttcatccatccaaaaagagt 129482

Score = 61.9 bits (31), Expect = 4e-06  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 630 tttgtcttactgttaagtcatacaagtgtctg 660  
|||||||  
Sbjct: 129361 tttgtcttactgttaagtcatacaagtgtctg 129391

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 931 tgggtttcttaataatgggattaaagctga 960  
|||||||  
Sbjct: 129962 tgggtttcttaataatgggattaaagctga 129991

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 901 ggtgtattgcatttgtcattgttggcat 930  
|||||||  
Sbjct: 129902 ggtgtattgcatttgtcattgttggcat 129931

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 871 cctttccatgtggtaactgatttaatga 900  
||||||||||||||||||||||||||||  
Sbjct: 129842 cctttccatgtggtaactgatttaatga 129871

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 841 tgtttctacagactgaccatactgatatt 870  
||||||||||||||||||||||||||||  
Sbjct: 129782 tgtttctacagactgaccatactgatatt 129811

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 781 atccagtaagttcataccagggtccccac 810  
||||||||||||||||||||||||||||  
Sbjct: 129662 atccagtaagttcataccagggtccccac 129691

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 751 agagaaccactccagaataacttccagaaaa 780  
||||||||||||||||||||||||||||  
Sbjct: 129602 agagaaccactccagaataacttccagaaaa 129631

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1167 tgtgttacctgctccagaaagaccttctca 1196  
||||||||||||||||||||||||  
Sbjct: 129572 tgtgttacctgctccagaaagaccttctca 129601

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1137 taaatggagttattcattcatcaaaaaaca 1166  
||||||||||||||||||||||||  
Sbjct: 129512 taaatggagttattcattcatcaaaaaaca 129541

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 691 tgggcctcaggtgaaactctctggcagcca 720  
|||||||  
Sbjct: 129482 tgggcctcaggtgaaactctctggcagcca 129511

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 661 agaaaacagacttgaagaaaatgagatgat 690  
|||||||  
Sbjct: 129422 agaaaacagacttgaagaaaatgagatgat 129451

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1077 cagaagtataagctgtggattgtccaacaa 1106  
|||||||  
Sbjct: 129392 cagaagtataagctgtggattgtccaacaa 129421

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1047 attgctagttcagtatattctgcccttagt 1076  
|||||||  
Sbjct: 129332 attgctagttcagtatattctgcccttagt 129361

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 601 ttccatacagaattgccttactatctcttt 630  
|||||||  
Sbjct: 129302 ttccatacagaattgccttactatctcttt 129331

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1017 gtatttatgtgttggatgactataaaaggcagtgttagatgactacagtatggat 1046  
||||||||||||||||||||||||||||||||  
Sbjct: 129272 gtatttatgtgttggatgactataaaaggcagtgttagatgactacagtatggat 129301

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 571 aacatttggttcagcattgctgagcagcag 600  
|||||||||||||||||||||||||||||||  
Sbjct: 129242 aacatttggttcagcattgctgagcagcag 129271

Score = 60.0 bits (30), Expect = 1e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 987 agtgttcacagtcttggaaacttcaaga 1016  
|||||||||||||||||||||||||||||||  
Sbjct: 129212 agtgttcacagtcttggaaacttcaaga 129241

Score = 54.0 bits (27), Expect = 0.001  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 961 gtaataattctcactgtttaccaagga 987  
|||||||||||||||||||||||||||  
Sbjct: 130022 gtaataattctcactgtttaccaagga 130048

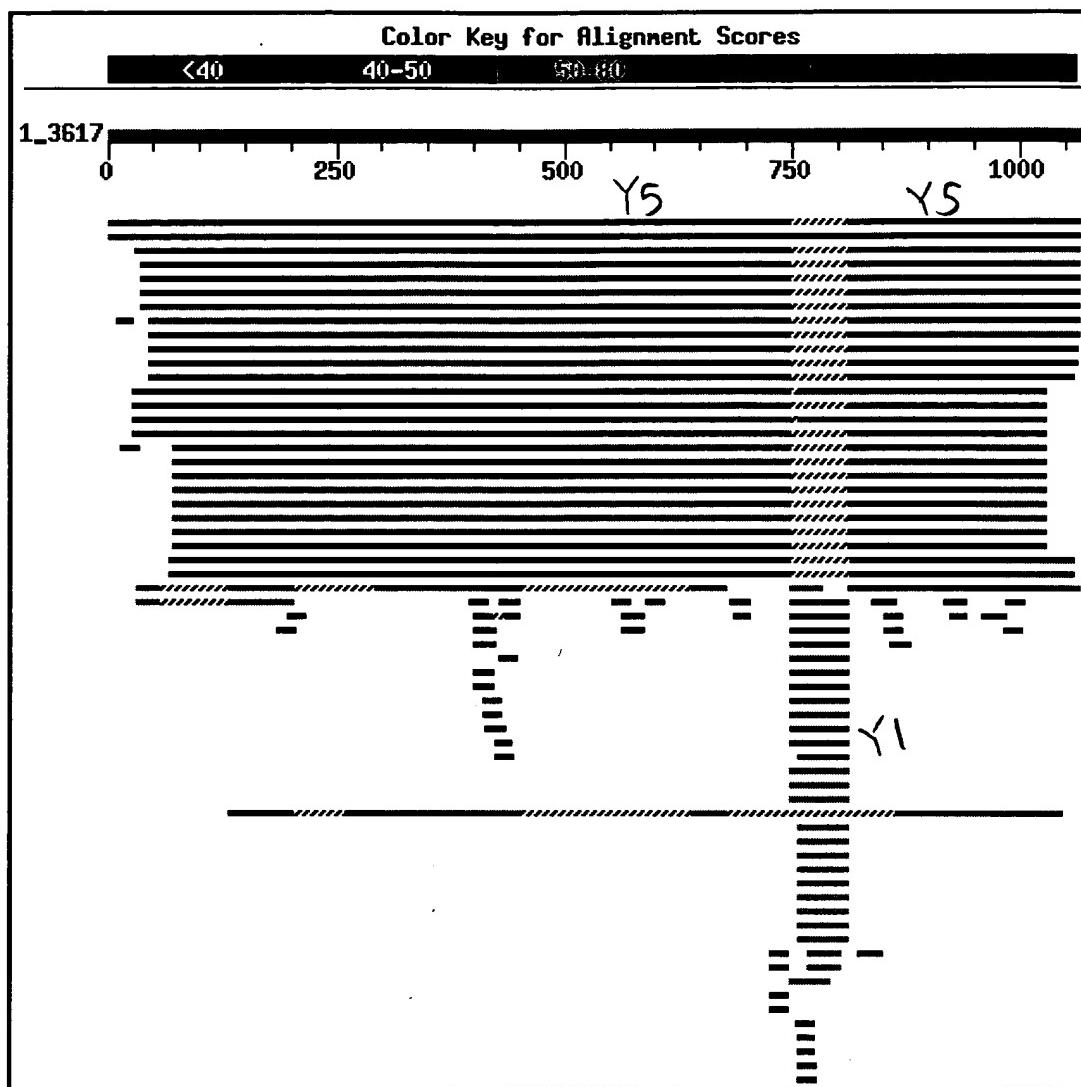
□>gi|1438903|gb|U56079.1|HSU56079 G|U Human Y5 receptor mRNA, complete cds  
Length = 1418

Score = 1132 bits (571), Expect = 0.0  
Identities = 571/571 (100%)  
Strand = Plus / Plus

Query: 1 ttttgggtgctgacaaatgtcttttattccaaggcaggactataatatggatggat 60  
|||||||||||||||||||||||||||||||||||||||  
Sbjct: 10 ttttgggtgctgacaaatgtcttttattccaaggcaggactataatatggatggat 69

Query: 61 cgacgagtattataacaagacacttgccacagagaataatactgctgccactcgaaattc 120  
|||||||||||||||||||||||||||||||||||  
Sbjct: 70 cgacgagtattataacaagacacttgccacagagaataatactgctgccactcgaaattc 129

Query: 121 tgatttcccagtctggatgactataaaaggcagtgttagatgactacagtatggat 180  
|||||||||||||||||||||||||||||||||||||||



Sequences producing significant alignments:

		Score (bits)	E Value
<u>gi 16756377 gb AC079238.7 </u>	Homo sapiens BAC clone RP11-719L...	<u>1459</u>	0.0
<u>gi 1438903 gb U56079.1 HSU56079</u>	Human Y5 receptor mRNA, com...	<u>1459</u>	0.0
<u>gi 1620655 gb U66275.1 HSU66275</u>	Human neuropeptide Y5 recep...	<u>1402</u>	0.0
<u>gi 22832895 gb BC034224.1 </u>	Homo sapiens neuropeptide Y rece...	<u>1386</u>	0.0
<u>gi 31377784 ref NM_006174.2 </u>	Homo sapiens neuropeptide Y re...	<u>1386</u>	0.0
<u>gi 27502795 gb BC042416.1 </u>	Homo sapiens neuropeptide Y rece...	<u>1386</u>	0.0
<u>gi 1945448 gb U94320.1 HSU94320</u>	Human neuropeptide Y5 recep...	<u>1386</u>	0.0
<u>gi 32481996 gb AY322538.1 </u>	Homo sapiens neuropeptide Y rece...	<u>1368</u>	0.0
<u>gi 11875769 gb AF303091.1 AF303091</u>	Macaca mulatta neuropept...	<u>1289</u>	0.0
<u>gi 50978823 ref NM_001003118.1 </u>	Canis familiaris neuropepti...	<u>971</u>	0.0
<u>gi 3169282 gb AF049328.1 AF049328</u>	Canis familiaris neuropep...	<u>971</u>	0.0
<u>gi 14029709 gb AF363240.1 AF363240</u>	Cavia porcellus NPY rece...	<u>932</u>	0.0
<u>gi 22476189 gb AC123796.2 </u>	Mus musculus BAC clone RP24-320P...	<u>692</u>	0.0
<u>gi 33942177 gb AC116731.9 </u>	Mus musculus chromosome 8, clone...	<u>692</u>	0.0
<u>gi 52839799 gb AC100541.17 </u>	Mus musculus chromosome 8, clon...	<u>692</u>	0.0

<u>gi 2564650 gb AF022948.1 AF022948</u>	Mus musculus neuropeptide...	692	0.0	G
<u>gi 26337480 dbj AK045587.1 </u>	Mus musculus adult male corpora...	692	0.0	GU
<u>gi 7710071 ref NM_016708.1 </u>	Mus musculus neuropeptide Y rec...	684	0.0	GIUE
<u>gi 6714644 dbj AB001346.1 </u>	Mus musculus mRNA for neuropepti...	684	0.0	GIUE
<u>gi 3169284 gb AF049329.1 AF049329</u>	Mus musculus neuropeptide...	684	0.0	GIUE
<u>gi 6981283 ref NM_012869.1 </u>	Rattus norvegicus neuropeptide ...	672	0.0	GIUE
<u>gi 1620657 gb U66274.1 RNU66274</u>	Rattus norvegicus neuropept...	672	0.0	GIUE
<u>gi 1438905 gb U56078.1 RNU56078</u>	Rattus norvegicus Y5 recept...	672	0.0	GU
<u>gi 3098509 gb AF044264.1 AF044264</u>	Rattus norvegicus neurope...	672	0.0	GIU
<u>gi 4249728 gb AF106083.1 AF106083</u>	Sus scrofa neuropeptide Y...	668	0.0	
<u>gi 3808059 dbj AB019185.1 </u>	Sus scrofa NPY Y5 gene for neuro...	668	0.0	
<u>gi 976208 gb L47169.1 HUMNPYAC</u>	Homo sapiens neuropeptide Y ...	460	e-126	
<u>gi 41350310 ref NM_000909.4 </u>	Homo sapiens neuropeptide Y re...	125	2e-25	GU
<u>gi 47939538 gb BC071720.1 </u>	Homo sapiens neuropeptide Y rece...	125	2e-25	GU
<u>gi 34194271 gb BC036657.2 </u>	Homo sapiens neuropeptide Y rece...	125	2e-25	GU
<u>gi 45239064 gb AY548168.1 </u>	Homo sapiens neuropeptide Y1 rec...	125	2e-25	GU
<u>gi 1430810 emb X99269.1 HSNPYY1</u>	H.sapiens NPYY1 gene	125	2e-25	G
<u>gi 189155 gb M88461.1 HUMNEYPEPY</u>	Human neuropeptide Y pepti...	125	2e-25	GIUE
<u>gi 189284 gb L07615.1 HUMNPYY1A2</u>	Human neuropeptide Y recep...	125	2e-25	GIUE
<u>gi 189153 gb M84755.1 HUMNEUYREC</u>	Human neuropeptide y recep...	125	2e-25	GIUE
<u>gi 11875765 gb AF303089.1 AF303089</u>	Macaca mulatta neuropept...	117	6e-23	
<u>gi 50950122 ref NM_001002930.1 </u>	Canis familiaris neuropepti...	109	1e-20	GU
<u>gi 2988393 gb AF005778.1 AF005778</u>	Canis familiaris neuropep...	109	1e-20	GIUE
<u>gi 5410445 gb AF135061.1 AF135061</u>	Cavia porcellus neuropept...	103	8e-19	
<u>gi 50746171 ref XM_420388.1 </u>	PREDICTED: Gallus gallus simil...	98	5e-17	G
<u>gi 47523647 ref NM_214288.1 </u>	Sus scrofa neuropeptide Y Y1 r...	96	2e-16	GU
<u>gi 6457647 gb AF106081.2 AF106081</u>	Sus scrofa neuropeptide Y...	96	2e-16	G
<u>gi 9789708 gb AF005779.2 AF005779</u>	Sus scrofa neuropeptide Y...	96	2e-16	GU
<u>gi 19548983 gb AY040844.1 </u>	Gallus gallus neuropeptide Y rec...	92	3e-15	
<u>gi 34877857 ref XM_344502.1 </u>	Rattus norvegicus neuropeptide...	76	2e-10	GU
<u>gi 30410855 gb BC051420.1 </u>	Mus musculus neuropeptide Y rece...	76	2e-10	GU
<u>gi 6754881 ref NM_010934.1 </u>	Mus musculus neuropeptide Y rec...	76	2e-10	GIUE
<u>gi 53442 emb Z18283.1 MMNPY1E03</u>	Mus musculus of NPY-1 recep...	76	2e-10	G
<u>gi 57636 emb Z11504.1 RRNPV1R</u>	R.rattus mRNA for NPY-1 receptor	76	2e-10	GE
<u>gi 53438 emb Z18280.1 MMNPY1CDS</u>	Mus musculus NPY-1 receptor	76	2e-10	GE
<u>gi 961479 dbj D63819.1 MUSNYY1RB</u>	Mouse mRNA for neuropeptid...	76	2e-10	GIUE
<u>gi 961477 dbj D63818.1 MUSNYY1RA</u>	Mouse mRNA for neuropeptid...	76	2e-10	GIUE
<u>gi 50746251 ref XM_426285.1 </u>	PREDICTED: Gallus gallus simil...	64	7e-07	G
<u>gi 19548985 gb AY040845.1 </u>	Gallus gallus neuropeptide Y rec...	64	7e-07	
<u>gi 409169 gb L25416.1 XELNPYPYY</u>	Xenopus laevis NPY/PYY rece...	64	7e-07	GU
<u>gi 46427829 emb CR389184.1 </u>	Gallus gallus finished cDNA, cl...	56	2e-04	U
<u>gi 33302262 gb AY177273.1 AY177272S2</u>	Squalus acanthias NPY ...	56	2e-04	
<u>gi 1480713 gb U62122.1 OAU62122</u>	Ovis aries Y1 neuropeptide ...	56	2e-04	GU
<u>gi 18425235 gb AC093027.12 </u>	Homo sapiens 12q BAC RP11-701B6...	48	0.042	
<u>gi 51988057 gb AC123647.9 </u>	Mus musculus chromosome 3, clone...	44	0.66	
<u>gi 51100952 dbj AB104827.2 </u>	Candida boidinii FGH1 gene for ...	44	0.66	
<u>gi 31746714 gb AC133101.4 </u>	Mus musculus BAC clone RP23-154M...	42	2.6	
<u>gi 37693674 gb AC121082.13 </u>	Mus musculus chromosome 7, clon...	42	2.6	
<u>gi 53379715 gb AC149588.4 </u>	Mus musculus chromosome 15 clone...	42	2.6	

<u>gi 52077841 gb AC132394.3 </u>	Mus musculus chromosome 6 clone ...	<u>42</u>	2.6	
<u>gi 49533628 gb AC115341.6 </u>	Rattus norvegicus 3 BAC CH230-24...	<u>42</u>	2.6	
<u>gi 20334476 gb AC079822.13 </u>	Homo sapiens 3 BAC RP11-413G22 ...	<u>42</u>	2.6	
<u>gi 20986479 gb AC084701.5 </u>	Homo sapiens chromosome 18, clon...	<u>42</u>	2.6	
<u>gi 2462139 emb Z70681.1 CEC30F2</u>	Caenorhabditis elegans cosm...	<u>42</u>	2.6	
<u>gi 28144384 gb AC008443.10 </u>	Homo sapiens chromosome 5 clone...	<u>42</u>	2.6	
<u>gi 27228882 gb AC104463.3 </u>	Homo sapiens chromosome 1 clone ...	<u>42</u>	2.6	
<u>gi 26080542 gb AC098934.3 </u>	Homo sapiens chromosome 1 clone ...	<u>42</u>	2.6	
<u>gi 4753229 gb AC006335.2 AC006335</u>	Homo sapiens BAC clone RP...	<u>42</u>	2.6	
<u>gi 15431133 gb AC013660.9 </u>	Homo sapiens, clone RP11-20A14, ...	<u>42</u>	2.6	
<u>gi 7408112 gb AC017019.3 AC017019</u>	Homo sapiens BAC clone RP...	<u>42</u>	2.6	
<u>gi 608510 gb U16311.1 BRU16311</u>	Brachydanio rerio homeodomai...	<u>42</u>	2.6	G U
<u>gi 26330583 dbj AK035302.1 </u>	Mus musculus adult male urinary...	<u>42</u>	2.6	G U
<u>gi 26084230 dbj AK034836.1 </u>	Mus musculus 12 days embryo emb...	<u>42</u>	2.6	G U
<u>gi 21655430 emb AL732316.10 </u>	Mouse DNA sequence from clone ...	<u>42</u>	2.6	
<u>gi 38678612 gb AC117702.10 </u>	Mus musculus chromosome 10, clo...	<u>40</u>	10	
<u>gi 17570664 ref NM_077495.1 </u>	Caenorhabditis elegans allatos...	<u>40</u>	10	G
<u>gi 22539392 gb AC114918.4 </u>	Mus musculus BAC clone RP23-86N2...	<u>40</u>	10	
<u>gi 33242564 gb AY336522.1 </u>	Sulfolobus solfataricus strain P...	<u>40</u>	10	
<u>gi 51854744 gb AC133187.3 </u>	Mus musculus chromosome 1 clone ...	<u>40</u>	10	
<u>gi 44844336 emb BX247953.2 </u>	Mouse DNA sequence from clone R...	<u>40</u>	10	
<u>gi 51233561 gb AC110499.19 </u>	Mus musculus chromosome 1, clon...	<u>40</u>	10	
<u>gi 50902420 gb CP000003.1 </u>	Streptococcus pyogenes MGAS10394...	<u>40</u>	10	
<u>gi 50761406 ref XM_424720.1 </u>	PREDICTED: Gallus gallus simil...	<u>40</u>	10	G
<u>gi 21904646 gb AE014155.1 </u>	Streptococcus pyogenes MGAS315, ...	<u>40</u>	10	
<u>gi 34786898 emb AL831812.5 CNS08CAP</u>	Oryza sativa chromosome...	<u>40</u>	10	
<u>gi 21535755 emb AL713907.3 CNS07YQ7</u>	Oryza sativa chromosome...	<u>40</u>	10	
<u>gi 33620400 emb AL929018.14 </u>	Mouse DNA sequence from clone ...	<u>40</u>	10	
<u>gi 21281541 gb AC104163.2 </u>	Homo sapiens chromosome 3 clone ...	<u>40</u>	10	
<u>gi 21206336 gb AC100868.2 </u>	Homo sapiens chromosome 8, clone...	<u>40</u>	10	
<u>gi 27228874 gb AC093576.3 </u>	Homo sapiens chromosome 1 clone ...	<u>40</u>	10	
<u>gi 51534200 emb BX530059.4 </u>	Zebrafish DNA sequence from clo...	<u>40</u>	10	
<u>gi 21104611 dbj AP003241.3 </u>	Oryza sativa (japonica cultivar...	<u>40</u>	10	
<u>gi 15623809 dbj AP003231.3 </u>	Oryza sativa (japonica cultivar...	<u>40</u>	10	
<u>gi 25137544 dbj AP005900.1 </u>	Homo sapiens genomic DNA, chrom...	<u>40</u>	10	
<u>gi 46240964 gb AC145942.4 </u>	Gallus gallus chromosome UNK clo...	<u>40</u>	10	

**Alignments**

[Get selected sequences](#)     [Select all](#)     [Deselect all](#)

>gi|16756377|gb|AC079238.7|     Homo sapiens BAC clone RP11-719L21 from 4, comple...  
Length = 142462

Score = 1459 bits (736), Expect = 0.0  
Identities = 750/752 (99%), Gaps = 2/752 (0%)  
Strand = Plus / Plus

Query: 1 ttttggtgctgacaaatgtcttttattccaaggcaggactataatatggatttagagct 60  
Sbjct: 128642 ttttggtgctgacaaatgtcttttattccaaggcaggactataatatggatttagagct 128701

Query: 61 cgacgagtattataacaagacacttgccacagagaataatactgctgccactcgaaattc 120

Sb1st: 128702 ggagggttataaaagaaacttggccatggaaataactgtggactcggattc 128761

Query: 121 tgattttccaaqtctqqqatqactataaaaqcaqtgttagatqacttacagtatTTCTGAT 180

Sbjct: 128762 tgattttccaaatgttggatgactataaaaagcaatgttagatgtactaacatgtatTTCTat 128821

Query: 181 tgggcctatacattgttaagtcttggcttatgggaatctacttatttaatggc 240

Sbjct: 128822 tgggctctatacattgttaagtcttcttggctttatggggaaatctaacttattttaatggc 128881

Query: 241 tctcatgaaaaagcgtaatcagaagactacggtaacttccataggcaatctggc 300

Sbjct: 128882 tctcataaaaagcgtaatcagaagactacggtaaacttcttcataaggcaatctggcctt 128941

Query: 301 ttctgatatctggtgtgtgtttgctcaccttacacactgacgtctgtttgctgga 360

Sbjct: 128942 ttctgatattctgggtgtcttttgcacactgacgtctgtcttgata 129001

Query: 361 tcagtggatgttggaaagtcatgtccatattatgcctttcttaatgtgtcagt 420

Sbjct: 129002 tcaqtqqatqtttqgcaaaqtcatqtqccatattatqcctttcttcataatqtgtgtcaqt 129061

Query: 421 tttgggttcaacttaatttaatataatcaattgcattgtcaggtatcatatgataaaaaca 480

Sbjct: 129062 ttttgttcaacttaatttaatatacattgcattgtcaggatcatatgataaaaca 129121

Query: 481 tccccatataatctaataatttacagcaaaccatggctactttctgatagctactgtctggac 540

Sbjct: 129122 tccccatataatctaataatttaacagcaaaaccatggctactttctgatagtactgtctggac 129181

Query: 541 actaggtttgccatctgttctcccccgtttcacagtcttgtggacttcaaga 600

Sbjct: 129182 actaagggtttggccatctgttctcccccttcagaqtttcacagtcttgaaacttcaaga 129241

Query: 601 aacatttggttcagcattgtc-aggcagcaggat-ttatgtgttgagtcatggccatctga 659

Sbjct: 129242 aacatttggtcagcattgtcgatgcaggatattatgttgtgatcatggccatctga 129301

Query: 660 ttcatacagaattgccttactatctctttattgtcttagt-tattctgcccttagt 718

Sbjct: 129302 ttccatacagaattgccttactatctctttatggtagttcgatattctggcccttagt 129361

Query: 719 . ttgtcttactgtaaatcataacaagtgtctgca 750

Sbjct: 129362 ttgtcttactgtaagtcatacaagtgtctgca 129393

Score = 505 bits (255), Expect = e-140  
 Identities = 255/255 (100%)  
 Strand = Plus / Plus

Query: 813 agatctcgaaagtgtttctacagactgaccatactgatatttagtatttgctgttagttgg 872  
 |||||||  
 Sbjct: 129771 agatctcgaaagtgtttctacagactgaccatactgatatttagtatttgctgttagttgg 129830

Query: 873 atgccactacaccccccattgtggtaactgatttaatgacaatcttatttcaaataagg 932  
 |||||||  
 Sbjct: 129831 atgccactacaccccccattgtggtaactgatttaatgacaatcttatttcaaataagg 129890

Query: 933 catttcaagttgggtattgcatttgtcattgtggcatgatgtccctgtgtcttaat 992  
 |||||||  
 Sbjct: 129891 catttcaagttgggtattgcatttgtcattgtggcatgatgtccctgtgtcttaat 129950

Query: 993 ccaattctatatgggttcttaataatgggattaaagctgatttagtgcacccctatacac 1052  
 |||||||  
 Sbjct: 129951 ccaattctatatgggttcttaataatgggattaaagctgatttagtgcacccctatacac 130010

Query: 1053 tgtcttcatatgtaa 1067  
 |||||  
 Sbjct: 130011 tgtcttcatatgtaa 130025

Score = 125 bits (63), Expect = 2e-25  
 Identities = 63/63 (100%)  
 Strand = Plus / Minus

Query: 750 atacgcctaaaaaggagaaacaacatgatggacaagatgagagagacaataagtacaggtcc 809  
 |||||||  
 Sbjct: 104166 atacgcctaaaaaggagaaacaacatgatggacaagatgagagagacaataagtacaggtcc 104107

Query: 810 agt 812  
 |||  
 Sbjct: 104106 agt 104104

>gi|1438903|gb|U56079.1|HSU56079 G|U Human Y5 receptor mRNA, complete cds  
 Length = 1418

Score = 1459 bits (736), Expect = 0.0  
 Identities = 750/752 (99%), Gaps = 2/752 (0%)  
 Strand = Plus / Plus

Query: 1 ttttgggtgctgacaaatgtcttttattccaaggcaggactataatggatggatagct 60  
 |||||||  
 Sbjct: 10 ttttgggtgctgacaaatgtcttttattccaaggcaggactataatggatggatagct 69

Query: 61 cgacgagtattataacaagacacttgcacagagaataatactgctgccactcgaaatc 120  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 70 cgacgagtattataacaagacacttgcacagagaataatactgctgccactcgaaatc 129

Query: 121 tgattcccagtcggatgactataaaagcagtgttagatgacttacagtatTTCTGAT 180  
||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 130 tgattcccagtcggatgactataaaagcagtgttagatgacttacagtatTTCTGAT 189

Query: 181 tgggctctatacattgttaagtcttcttggtttatgggaatctacttattttatggc 240  
||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 190 tgggctctatacattgttaagtcttcttggtttatgggaatctacttattttatggc 249

Query: 241 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300  
||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 250 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 309

Query: 301 ttctgatatcttgggtgtgctgtttgctcaccttacactgacgtctgtcttgatgg 360  
||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 310 ttctgatatcttgggtgtgctgtttgctcaccttacactgacgtctgtcttgatgg 369

Query: 361 tcagtgatgtttggcaaagtcatgtccatattatgcctttttcaatgtgtcagt 420  
||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 370 tcagtgatgtttggcaaagtcatgtccatattatgcctttttcaatgtgtcagt 429

Query: 421 ttgggttcaacttaatttatcaattgccattgtcaggtatcatatgataaaaca 480  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 430 ttgggttcaacttaatttatcaattgccattgtcaggtatcatatgataaaaca 489

Query: 481 tcccatatctaataatttaacagcaaaccatggctacttctgatagctactgtctggac 540  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 490 tcccatatctaataatttaacagcaaaccatggctacttctgatagctactgtctggac 549

Query: 541 actagggtttgcacatgtttctcccttccagtgtttcacagtctgtggacttcaaga 600  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 550 actagggtttgcacatgtttctcccttccagtgtttcacagtctgtggacttcaaga 609

Query: 601 aacatttggttcagcattgct-agcagcaggtatTTTGTGTTGAGTCATGGCCATCTGA 659  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 610 aacatttggttcagcattgctgagcagcaggtatTTTGTGTTGAGTCATGGCCATCTGA 669

Query: 660 ttcatacagaattgccttactatctcttattgcttagttcagt-tattctGCCCTTAGT 718  
||||||||||||||||||||||||||||||||||||  
Sbjct: 670 ttcatacagaattgccttactatctcttattgcttagttcagtatattctGCCCTTAGT 729

Query: 719 ttgtcttactgtaaGTcatacAGTGTCTGCA 750  
||||||||||||||||||||||||  
Sbjct: 730 ttgtcttactgtaaGTcatacAGTGTCTGCA 761

\*RID=1098303226-3617-14352993012.BLASTQ4,

Score = 505 bits (255), Expect = e-140  
Identities = 255/255 (100%)  
Strand = Plus / Plus

Query: 813 agatctcgaagtgtttctacagactgaccatactgatatttagtatttgcgtttagttgg 872  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1139 agatctcqaagtgtttctacagactqaccatactqatatttagtatttgcgtttagttgg 1198

Query: 873 atgccactacaccctttccatgtggtaactgatttaatgacaatcttatttcaaataagg 932  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1199 atgccactacaccctttccatgtggtaactgatttaatgacaatcttatttcaaataagg 1258

Query: 933 catttcaagtgggtattgcatttgtcattgtgggcatgatgtccgttgtcttaat 992  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1259 catttcaagtqqtattqcatttgtcattttqqqcatqatgtccgttgtcttaat 1318

Query: 993 ccaattctatatgggttcttaataatgggattaaagctgatttagtgtccctatacac 1052  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 1319 ccaattctatatgggttcttaataatgggattaaagctgatttagtgtccctatacac 1378

Query: 1053 tgtcttcatatgtaa 1067  
          |||||||||||||||  
Sbjct: 1379 tgtcttcatatgtaa 1393

>gi|1620655|gb|U66275.1|HSU66275 G|U Human neuropeptide Y5 receptor (NPYR5) mRNA  
Length = 1370

Score = 1402 bits (707), Expect = 0.0  
Identities = 721/723 (99%), Gaps = 2/723 (0%)  
Strand = Plus / Plus

Query: 30 ccaaggcaggactataatggatttagagctcgacgagtattataacaagacacttgcca 89  
|||||||  
Sbjct: 1 ccaaqcaggactataatggatttagagctcgacgagtattataacaagacacttgcca 60

Query: 90 cagagaataatactgctgccactcggatttgcattccaggcttggatgactataaaa 149  
Sbjct: 61 cagagaataatactgctgccactcggatttgcattccaggcttggatgactataaaa 120

Query: 150 qcagtgttagatgacttacagttttctgattggctatacatattgttaagtcttc 209  
Sbjct: 121 qcagtgttagatgacttacagttttctqattggctatacatattgttaagtcttc 180

Query: 210 gcttatgggaatctacttatttaatggctctcataaaaagcgtaatcagaagacta 269  
||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 181 gcttatgggaatctacttatttaatggctctcataaaaagcgtaatcagaagacta 240

RID=1098303226-3617-14352993012.BLASTQ4,

Query: 270 cggtaaaactcctcataggcaatctggcctttctgatatcttgggtgtgtgtttgtc 329  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 241 cggtaaaactcctcataggcaatctggcctttctgatatcttgggtgtgtgtttgtc 300

Query: 330 cacccacactgacgtctgtcttgcgtggatcagtggatgtttggcaaagtcatgtgcc 389  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 301 cacccacactgacgtctgtcttgcgtggatcagtggatgtttggcaaagtcatgtgcc 360

Query: 390 atattatgcctttcttcaatgtgttcagttggttcaacttaatttaatataaa 449  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 361 atattatgcctttcttcaatgtgttcagttggttcaacttaatttaatataaa 420

Query: 450 ttgccattgtcaggtatcatatgataaaacatcccataatctaataatttaacagcaaacc 509  
||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 421 ttgccattgtcaggtatcatatgataaaacatcccataatctaataatttaacagcaaacc 480

Query: 510 atggctactttctgatacgactactgtctggacacttaggtttgcacatctgttctcccttc 569  
||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 481 atggctactttctgatacgactactgtctggacacttaggtttgcacatctgttctcccttc 540

Query: 570 cagtgttcacagtctgtgaaacctcaagaaacattgggtcagcattgc-aggcaga 628  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 541 cagtgttcacagtctgtgaaacctcaagaaacattgggtcagcattgcgaggcaga 600

Query: 629 ggtatttatgtgttgagtcatggccatctgattcatacagaattgccttactatcttt 688  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 601 ggtatttatgtgttgagtcatggccatctgattcatacagaattgccttactatcttt 660

Query: 689 tattgctagttcagt-tattctgcccttagttgtcttactgttaagtcatacaagtgtct 747  
||||||||||||| ||||||||||||||||||||||||||  
Sbjct: 661 tattgctagttcagtatattctgcccttagttgtcttactgttaagtcatacaagtgtct 720

Query: 748 gca 750  
|||  
Sbjct: 721 gca 723

Score = 505 bits (255), Expect = e-140  
Identities = 255/255 (100%)  
Strand = Plus / Plus

Query: 813 agatctcgaaagtgtttctacagactgaccatactgatatttagtattgtgttagtgg 872  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 1101 agatctcgaaagtgtttctacagactgaccatactgatatttagtattgtgttagtgg 1160

Query: 873 atgccactacacccatgtggtaactgatttaatgacaatcttattcaaatagg 932  
||||||||||||||||||||||||||||||||||||  
Sbjct: 1161 atgccactacacccatgtggtaactgatttaatgacaatcttattcaaatagg 1220

Query: 933 catttcaagttggtgtattgcatttgtcattgttggcatgatgtcctgttgcattaaat 992  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1221 catttcaagttggtgtattgcatttgtcattgttggcatgatgtcctgttgcattaaat 1280

Query: 993 ccaattctatatggtttcttaataatgggattaaagctgatttagtgcacccattacac 1052  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1281 ccaattctatatggtttcttaataatgggattaaagctgatttagtgcacccattacac 1340

Query: 1053 tgtcttcataatgtaa 1067  
           |||||||||||||||  
 Sbjct: 1341 tgtcttcataatgtaa 1355

>gi|22832895|gb|BC034224.1| GI Homo sapiens neuropeptide Y receptor Y5, mRNA (c  
 IMAGE:4838926), partial cds  
 Length = 3197

Score = 1386 bits (699), Expect = 0.0  
 Identities = 713/715 (99%), Gaps = 2/715 (0%)  
 Strand = Plus / Plus

Query: 38 gactataatatggatttagagctcgacgagtattataacaagacacttgccacagagaat 97  
           ||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1514 gactataatatggatttagagctcgacgagtattataacaagacacttgccacagagaat 1573

Query: 98 aatactgctgccactcgaaattctgatttcccagtcggatgactataaaagcagtgt 157  
           ||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1574 aatactgctgccactcgaaattctgatttcccagtcggatgactataaaagcagtgt 1633

Query: 158 gatgacttacagtatttctgattggctctatacattgttaagtcttctggctttatg 217  
           ||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1634 gatgacttacagtatttctgattggctctatacattgttaagtcttctggctttatg 1693

Query: 218 gggaatctacttatttaatggctctcataaaaagcgtaatcagaagactacggtaaac 277  
           ||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1694 gggaatctacttatttaatggctctcataaaaagcgtaatcagaagactacggtaaac 1753

Query: 278 ttcctcataggcaatctggcctttctgatatcttgggtgtgtgtttgctcaccttc 337  
           ||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1754 ttcctcataggcaatctggcctttctgatatcttgggtgtgtgtttgctcaccttc 1813

Query: 338 acactgacgtctgtcttgcgtggatcagtggatgtttggcaaagtcatgtccatattatg 397  
           ||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1814 acactgacgtctgtcttgcgtggatcagtggatgtttggcaaagtcatgtccatattatg 1873

Query: 398 cctttcttcaatgtgtcagtttggttcaacttaatttaatcaattgccatt 457  
           ||||||||||||||||||||||||||||||||||||  
 Sbjct: 1874 cctttcttcaatgtgtcagtttggttcaacttaatttaatcaattgccatt 1933